

Gencore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 03:00:20 ; Search time 318.707 Seconds  
(without alignments)  
4571.527 Million cell updates/sec

Title: US-09-001-737-7

Perfect score: 1661  
Sequence: 1 GAAATCGGCTCATATGCA.....TGGCGGATAGACGCAATTC 1661

Scoring table: IDENTITY: NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 43858390 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications: NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCF\_NEM\_PUB.seq:\*
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- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEM\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1038.4	63.5	9	US-10-267-311-50
2	942.6	56.7	10	US-09-070-927A-42
3	615.8	37.1	10	US-09-790-988-1
4	589.8	35.5	10	US-09-650-438-13
5	530.4	31.9	10	US-09-841-132-180
6	483.6	29.1	7	US-08-781-968A-266
7	464.2	27.9	1614	US-09-738-626-565
8	461.6	27.8	2847	US-10-267-311-20
9	460.0	27.8	1947	US-10-267-311-20
10	458.6	27.6	1947	US-10-267-311-28
11	458.6	27.6	1623	US-09-712-363-23
12	458.6	27.6	1920	US-10-267-311-16
13	458.4	27.6	3309400	US-09-738-626-2986
14	457.2	27.5	2130	US-10-068-059-7
15	457.0	27.5	1644	US-09-738-626-2986
16	456.4	27.5	2241	US-10-068-059-5
17	456.2	27.5	2175	US-10-068-059-11
18	455.6	27.4	2073	US-10-068-059-9
19	453.4	27.3	1736	US-10-007-693-19

## ALIGNMENTS

20	446.8	26.9	1526	9	US-10-051-643-159	Sequence 159, App
21	446.8	26.9	1626	9	US-09-880-505-159	Sequence 159, App
22	446.2	26.9	1734	9	US-09-880-842A-2463	Sequence 2463, App
23	444.8	26.8	1569	9	US-10-051-643-113	Sequence 113, App
24	444.8	26.8	1569	9	US-09-880-505-113	Sequence 113, App
25	419.4	25.2	1761	9	US-09-880-842A-216	Sequence 216, App
26	411.4	24.8	2360	10	US-09-834-975-774	Sequence 774, App
27	401.4	24.2	1575	10	US-09-338-842A-1653	Sequence 1653, App
28	395.0	21.4	783	10	US-09-974-300-1947	Sequence 1947, App
29	337.8	20.3	1944	9	US-10-267-311-52	Sequence 52, App
30	300.6	18.1	1158	9	US-09-738-626-667	Sequence 667, App
31	273.8	16.5	985	9	US-10-051-643-161	Sequence 161, App
32	273.8	16.5	985	9	US-09-880-505-161	Sequence 161, App
33	271.8	16.4	927	9	US-10-051-643-116	Sequence 116, App
34	271.8	16.4	927	9	US-09-880-505-116	Sequence 116, App
35	256.6	15.7	565	10	US-09-974-300-6342	Sequence 6342, App
36	256.6	15.4	772	12	US-10-007-693-113	Sequence 113, App
37	247.0	14.9	525	10	US-09-974-300-6303	Sequence 6303, App
38	198.8	12.0	644	7	US-08-781-968A-797	Sequence 797, App
39	176.6	10.6	647	9	US-10-051-643-115	Sequence 115, App
40	176.6	10.6	647	9	US-09-880-505-115	Sequence 115, App
41	173.4	10.4	888	9	US-10-267-311-32	Sequence 32, App
42	162.2	9.8	400	10	US-09-974-300-6301	Sequence 6301, App
43	149.6	9.0	630	10	US-09-998-598-744	Sequence 744, App
44	145.6	8.8	256	10	US-09-974-300-1987	Sequence 1987, App
45	132.6	8.0	406	10	US-09-925-301-701	Sequence 701, App

RESULT 1  
US-10-267-311-50  
Sequence 50, Application US/10267311  
Publication NO US200305046581

GENERAL INFORMATION:  
APPLICANT: Siegel, Marvin  
APPLICANT: Chu, N. Randall  
APPLICANT: Mizen, Lee A.  
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
FILE REFERENCE: 12071/002001  
CURRENT FILING DATE: US/10/267.311  
PRIOR APPLICATION NUMBER: US/09/613.303  
PRIOR FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: US 60/143.757  
PRIOR FILING DATE: 1999-07-08  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 50  
LENGTH: 1926  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion sequence  
NAME/KEY: CDS  
LOCATION: (1)...(1923)  
US-10-267-311-50

Query Match 62.5% ; Score 1038.4 ; DB 9 ; Length 1926 ;  
Best Local Similarity 77.5% ; Pred. No. 2.2e-244 ;  
Matches 158 ; Conservative 0 ; Mismatches 366 ; Indels 0 ; Gaps 0 ;

QY 15 ATGCGAAGAAATCAATTTTCAGAGATGCGGCTCTCCATGTCGCGAGTTGAT 74  
DB 1 ATGCGAAGAAATCAATTTTCAGAGATGCGGCTCTCCATGTCGCGAGTTGAT 60  
QY 75 ATGTTAGCAGATCCGTCAGTAGACGTCGTCCTTAAGGCGCAATGTTGTTGAA 134  
DB 61 ATCCCTGCACATACGTTAAAGTAACTTTGGGACCAAAAGCGCAATGCTGTTGAA 120  
QY 135 AAGCTTTTGCTTCCTTAACTTAAATGACGGGTAACCATTTGCTAAAGATCGAA 194

121 AAGTCATGCTGTCACCTGATGATTCACATGAGCGGTGACTATTGGCAAAATGAA 180  
195 TTAAAGATCATTTTGAACATGGAGCAAAATTTGTGTGATGAGCTTCTAAAC 254  
181 TTAAAGATCATTTTGAACATGGAGCAAAATTTGTGTGATGAGCTTCTAAAC 240  
225 AATGATATGCTGCTGATGAGCACTACTGCAACAGTTTGGACAGCACTTGTTCAT 314  
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361 ACAGCAACGCAAGCAGCTGTGAACCTTGAACCCATCTCTCATCCTGATCTGCAAC 420  
435 GAAGGATATGCTGCTGATGAGCACTACTGCAACAGTTTGGACAGCACTTGTTCAT 494  
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555 ATGGAACGAGCACTGATGAGTGTGAGCAATTTGACGCTGCTGCTGCA 614  
541 ATGGAACGAGCACTGATGAGTGTGAGCAATTTGACGCTGCTGCTGCA 600  
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601 TACATGCTCAGACATGAAAAATGTTGCGACCTGAAACCATTTACTTATC 660  
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661 ACGGATAAAAAGTCAACATGCAAGCACTTTGCGACCTGAAACCATTTACTTATC 720  
735 ACCAAGCTCCTACTCTATTGTCAGATGATGATGATGATGATGATGATGATGATGAT 794  
721 ACCAAGCTCCTACTCTATTGTCAGATGATGATGATGATGATGATGATGATGATGAT 780  
795 GTCTGGAACAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 854  
781 GTCTGGAACAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
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841 GATGCTGTAAGCTATGCTGTAAGCAATGCTATCTGACAGCTGATGATGATGATGATGAT 900  
915 GATGCTGTAAGCTATGCTGTAAGCAATGCTATCTGACAGCTGATGATGATGATGATGAT 974  
901 GATGCTGTAAGCTATGCTGTAAGCAATGCTATCTGACAGCTGATGATGATGATGATGAT 960  
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961 ATTACAGTGTAAAGATGACAGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
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1141 GCTCCACAGACAGCTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
1215 ACAGCTGACAGCTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1274

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1321 CTGCTGCTGTTGAAGAAGTATTGTCAGAGTGTGGAACAGCTCTTGGCAATG 1380  
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1575 AAACCTGACAGCTAGAGCGGAGCAGCATGATGATGATGATGATGATGATGATGATGATGAT 1634  
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1635 GCTG 1638  
1621 GGAG 1624

RESULT 2  
US-09-070-927A-42  
Sequence 42, Application US/09070927A  
Patent No. US20020120116A1  
GENERAL INFORMATION:  
APPLICANT: Charles A. Kunach  
Patrick J. Dillon  
Steven Barash  
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070, 927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,655  
FILING DATE: 1997-05-16  
APPLICATION NUMBER: 60/044,031  
FILING DATE: 1997-05-06  
APPLICATION NUMBER: 60/066,009  
FILING DATE: 1997-11-14  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB369  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:

Wed Apr 16 08:05:36 2003

us-09-001-737-7.rmpb

Page 3

LENGTH: 3625 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
us-09-070-927A-42

Query Match 56.7% Score 942.6 DB 10: Length 3625;  
Best Local Similarity 74.2% Pred. No. 8.9e-221;  
Matches 1191; Conservative 0; Mismatches 415; Indels 0; Gaps 0;

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OY 75 ATGTAGCAGATACCGTCAAAAGTACCTTGTCTTAAAGGCGCAATGTTCTTGA 134  
Db GTATTAGCAGATACGTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 483  
OY 135 AAAGCTTTGGTCTGCTTAATTAATGACGGGGTAACCAATGCTTAAGAGATGGA 194  
Db AAATCATTTGGTCTGCTTAATTAATGACGGGGTAACCAATGCTTAAGAGATGGA 543  
OY 195 TTGAAAGATCTTTTAAACATGCGAGCAAAATTTGGTCTTAAAGGCGCAATG 254  
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OY 255 AATGATATGCTGCTGAGTGGAGACACTACTGCAACAGTTTGAACAGCAATTTTCAT 314  
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OY 315 GAAGCACTAAAAATGTGACAGCAGTGTGTAATCCATTTGGTCTGAGCAGATTGA 374  
Db GAAGCACTAAAAATGTGACAGCAGTGTGTAATCCATTTGGTCTGAGCAGATTGA 723  
OY 375 ACAGCAACAGCAACAGCTGTTGAAGCTTGAAGCAATTTGACCTGCTTACCTGCTCAA 434  
Db TTAGCAACAAAAACAGCAAGTGAAGATTAACAAATTTTCATCTGCTGCTTACCTCAA 783  
OY 435 GAAGCTATGCTGAGTGGCGAGTATGATGACAGCTTGAAGAGTGGAGATATAC 494  
Db GAAGCTATGCTGAGTGGCGAGTATGATGACAGCTTGAAGAGTGGAGATATAC 843  
OY 495 TCAGAGCTATGAGAGCTGTGGCAAGATGCTGATTAACATGCAAGAAATTCGAGT 554  
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OY 555 ATGGAACAGAACTTGAAGTGTGGAAGGCAATTTGACCTGCTTACCTGCTCAA 614  
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OY 615 TACATGCTCAGACAGCAATGAAATTTGTTGCAAGCTTGAAGAGTGGAGTAAAC 674  
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Db ACCGCAAAAATTCGCAAAATTCGCAAGCAATTTGCAATGAGAGTGGTAA 1083  
OY 735 ACCAAGCGTCAATGCTATGATTTGAGAGATGAGATGAGAGCAATTCAGACCT 794  
Db CAAAGCGTCAATGCTATGATTTGAGAGATGAGATGAGAGCAATTCAGACCT 1143  
OY 795 GCTTGAAGCAAGATGCTGCTGCTTCAATGCTGCTGCTCAAGCGCGAGATTTGCT 854  
Db GTATTGAAGCAAGATGCTGCTGCTTCAATGCTGCTGCTCAAGCGCGAGATTTGCT 1203  
OY 855 GATGCTGTAAGCTATGCTTGAAGCAATGCTTGAAGCAAGTGTGAGATGATTA 914  
Db GATGCTGTAAGCTATGCTTGAAGCAATGCTTGAAGCAAGTGTGAGATGATTA 1263  
OY 915 GAGATCTAGACTTGAATTAAGATGCTCAATGACAGCTTGAAGCGCTGATAG 974  
Db GAGATCTAGACTTGAATTAAGATGCTCAATGACAGCTTGAAGCGCTGATAG

Db 1264 GACGACTAGAGGTTAGATTAAAAAGCAACATTTGAAAACTTACGAATGCTGCAAA 1323  
OY 975 ATTCAGATTGATTAAGATACGACGATTAATTTGGAAGTTCAGAGATTCAGAACTTAT 1034  
Db GTAGTTGATGCAAGAAAGATTAACCAATTTGCTGAGATGCTGCTGCTGCTGCTGCTG 1383  
OY 1035 GCTAACGTAATGCTGATTAATGCAATTAAGAAACCAACTGCTGACTTGAAGCT 1094  
Db GATGCCCGGCTGATTAATTAATTAACCAATGCGGGAACCACTGCTGATTTGATGCT 1443  
OY 1095 GAAAACTACAGAAAGCTTTGGCAAAATTAAGTGGTGGTGGTGGTGGTGGTGGTGGT 1154  
Db GAAAACTACAGAAAGCTTTGAGTAAATTAATTAAGTGGTGGTGGTGGTGGTGGTGGT 1503  
OY 1155 GCTCCAGACAGACGCTTAAAGAAATGAATGCAATGCTGAGATGCTGCTAAATGCT 1214  
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OY 1215 ACAGCTGACGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1274  
Db ACAGCTGACGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1623  
OY 1275 ATGGAAGAGTACGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1334  
Db ATGGAAGAGTACGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683  
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Db CTTCGCTGCTGAGAGAGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743  
OY 1395 GTAGTTATGACAAATGTAAGAAAGAGCTTGAAGAGTATGCTGCTGCTGCTGCTG 1454  
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OY 1455 GAGTGGTGAATGATTAAGAAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1514  
Db GAGTGGTGAATGATTAAGAAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1863  
OY 1515 CTTCGCTGCTGAGAGAGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 1574  
Db CTTCGCTGCTGAGAGAGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1923  
OY 1575 AAACCTGAACAGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
Db AAACCTGAACAGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1969

RESULT 3  
US-09-790-988-1  
Sequence 1. Application US/09790988  
Patent No. US20020127687A1  
GENERAL INFORMATION:  
APPLICANT: SHIGEMBU, SHUJI  
APPLICANT: MATSUMOTO, HIROKI  
APPLICANT: MATSUMOTO, MASAHISA  
APPLICANT: SAKAKI, YOSHIYUKI  
TITLE OF INVENTION: GENE DNA OF BACTERIAL SYMBIONT OF APHIDS  
FILE REFERENCE: 081356/0159 US/09/790,988  
CURRENT APPLICATION NUMBER: US/09/790,988  
PRIORITY FILING DATE: 2001-02-23  
PRIORITY FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 640681  
TYPE: DNA  
ORGANISM: Buchnera sp.  
US-09-790-988-1  
Query Match 37.1% Score 615.8 DB 10: Length 640681;  
Best Local Similarity 62.8% Pred. No. 1.5e-139;  
Matches 991; Conservative 0; Mismatches 582; Indels 6; Gaps 2;

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OY 18 GCMAAAGAAATCAATTTTCAGCAGATGCGGCTGCTCCATGTCGCGGAGTTGATNG 77
DB 18721 GCTAAATATTAATTAATTTGCAATGAAAGCCGCAATTAATCTTCGAGGATATATGTA 18780
OY 78 TTACGAGATACCGTCAAAAGTAAAGTGTGCTGCTCAAAAGGCGCAATGTTGCTTGAATA 137
DB 18781 TTACGAGATACCGTCAAAAGTGTGCTGCTCAAAAGGCGCAATGTTGCTTGAATA 18840
OY 138 GCTTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 197
DB 18841 TCTTTGAGACACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 18900
OY 198 GAATATATTTTGAAGAAATGAGGCAAAATTTGCTGCTGAAGTGTCTTGAAGCAAT 257
DB 18901 GAATATATTTTGAAGAAATGAGGCAAAATTTGCTGCTGAAGTGTCTTGAAGCAAT 18960
OY 258 GATATGCTGCTGATGAGGAGCTACTGCAACAGTTTGTACCAAGCCATTTGTTGATGA 317
DB 18961 GATGACACGAGTGTGATGAGGAGCTACTGCAACAGTTTGTACCAAGCCATTTGTTGATGA 19020
OY 318 GGAATTAATAATGTGACGAGGCTGCTAATGCTAATGCTGATGCTGAGGAGCATTAACA 377
DB 19021 GGTATTAATAATGTGACGAGGCTGCTAATGCTAATGCTGATGCTGAGGAGCATTAACA 19080
OY 378 GCAACACCAACAGCTGCTGTAAGCCCTTGAAGCCATTTGCTCAACGCTGATGCTGAAGAA 437
DB 19081 GCTGCTATGCTGCTGCTGTAAGCCCTTGAAGCCATTTGCTCAACGCTGATGCTGAAGAA 19140
OY 438 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
DB 19141 GCAATTAACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19200
OY 495 TCAGAGCTATGAGAGCTGTGAGGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554
DB 19201 GCAGAGCTATGAGAGCTGTGAGGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19260
OY 555 ATGGAACAGAGCTGTAAGTGTGAGGCAACATTTGACCGTGTGCTGCTGCTGCTGCTGCT 614
DB 19261 TTACGAGATGAACTGTAAGTGTGCAAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19320
OY 615 TACATGCTGACAGCAATGAAAGTGTGCTGAGACCTTGAAGCCATTTGCTTATTC 674
DB 19321 TATTTATCAATTAACCAAGAGTGTGCTGAGACCTTGAAGCCATTTGCTTATTC 19380
OY 675 ACGGATTAATAAGTGTCAACATCCAGACATTTTCCACTACTGCTGAGAGAGTCTTAA 724
DB 19381 GCTATTAATAAGTGTCAACATCCAGACATTTTCCACTACTGCTGAGAGAGTCTTAA 19440
OY 725 ACGACCGCTCATTTATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 794
DB 19441 TCAGAGAAACCACTATTAATTTCTGAGATTTAGAGAGTGTGATGATGATGATGATGAT 19500
OY 795 GCTTGAACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
DB 19501 GCTATTAATTAAGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19560
OY 855 GATGCTGCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
DB 19561 GATGCTGCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19620
OY 915 GAGGATCTAGGATTTGAATTAAGATGCTCAATGACAGCCCTTGAAGAGGCTGCTAAG 974
DB 19621 GAGGATTTAGGATTTGAATTAAGATGCTCAATGACAGCCCTTGAAGAGGCTGCTAAG 19680
OY 975 ATTACGCTGTAAGATGACAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1034
DB 19681 GTTGTATTAAGCAAGACCTACACTATTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19740
OY 1035 GCTTACCGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094
DB 19741 CAAGAGCTGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 19800

OY 1095 GAAAGTACAGAGCTTTGCGAAGTAAATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1154
DB 19801 GAAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 19860
OY 1155 GCTCCACAGAGCTGCTTTAAAGAAATGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1214
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OY 1215 ACAGTGCAGCTGCTGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1274
DB 19921 ACAGTGCAGCTGCTGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19980
OY 1275 ATTGAAGAAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1331
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DB 20041 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20100
OY 1392 TCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1451
DB 20101 TCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20160
OY 1452 GGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1511
DB 20161 GGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20220
OY 1512 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1571
DB 20221 GCTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20280
OY 1572 AATAACCTGACAGCTTA 1590
DB 20281 GACTTGCTTAAGAGATA 20299

RESULT 4
US-09-960-428-13
: Sequence 13, Application US/09960428
: Patent No. US20020115147A1
: GENERAL INFORMATION:
: APPLICANT: Roche Diagnostics GmbH
: TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokary
: FILE REFERENCE: 5272/00/
: CURRENT APPLICATION NUMBER: US/09/960,428
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 13
: LENGTH: 2155
: TYPE: DNA
: ORGANISM: Escherichia coli
US-09-960-428-13

Query Match 35.5%; Score 589.8; DB 10; Length 2155;
Best Local Similarity 61.3%; Pred. No. 1,7e-134;
Matches 986; Conservative 0; Mismatches 617; Indels 6; Gaps 2;

```

Db 658 GAAGACAAGTTCGAAATATGGCTGCGACATGGTGAAGAAAGTTCCTCTAAAGCAAC 717  
 Oy 258 GATATTGCTGTGATGAGACGACTACGCAACGTTTGAACACAGCCATTGTCATGAA 317  
 Db 718 GAGCGTGAAGCGGAGTACACACGCTGACACGCTGACGCTGACGCTGACGCTGAA 777  
 Oy 318 GCACTAAAAATGTGACAGCAGTGTCTAATTCATGATTCCTGAGGAGCTTGAACA 377  
 Db 778 GGTCTGAAGAGTGTCTGCTGGGCAATGACCCGATGAGACGTAAGAGCTGTGACAAA 837  
 Oy 378 GCAGAGCAACAGCTGTGAAACCTTGAAGCCATTGCTCAACCTGTATCTGGCAAGAA 437  
 Db 838 GCGGTTACCGCTGCTGATGAAAGAAAGCCGCTGCGTACCATGCTCTGACTCTAAA 897  
 Oy 438 GCTATTGCTCAGTGTGCTGACATCATCAGCTC---TGAAGAAAGTGGAGAGATATC 494  
 Db 898 GCGATTGCTCAGTGTGCTGACATCTCCGTAACCTCGAAGAAACCTGATGATGATC 957  
 Oy 495 TCAGAAAGCTATGAGAGGCTGTGGGCAAGATGATGATGATGATGATGATGATGAT 554  
 Db 958 GCTGAAGGATGAGCAAAAGTGGGTAAGAGGCTTATCAGCTGTAAGAGAGCTACCGGT 1017  
 Oy 555 ATGGAACAGACATGTAAGTGTGAAAGGCAATTTGACCGTGTACCTGTCTCAA 614  
 Db 1018 CTGACAGAGCACTGAGCTGTGAAAGTGTGAGCTGCAACGCTGCTGCTCTCT 1077  
 Oy 615 TACATGTCACAGACATGAAATGTTGACAGCTTGAAGAAACCATTTATCTTATC 674  
 Db 1078 TACTTCATCAACAGCGGAAAGTGGCGAGTAAGAAAGCCGCTGATCTCTCTG 1137  
 Oy 675 ACGGATAAAAAGTGTCAAAAGTTCGAAAGATTTGCCACTGTAGAGATTTCTAAA 734  
 Db 1138 GCTGACAGAAATATCTCCAACTCCGCAAAAGTGTGCGGTTCTGGAACGTTGCCAAA 1197  
 Oy 735 ACCAAGCGCTCAATCTCATTTATGAGATGATGATGATGATGATGATGATGATGAT 794  
 Db 1198 GCAGCAAAACCGCTGCTGATCTGCTGAAGATGTAAGAAAGCAACGCTGCAACTCTG 1257  
 Oy 795 GTCTTGAAACAAGATGCTGCTGATCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTG 854  
 Db 1258 GTTGTAAACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317  
 Oy 855 GATCGTGTAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914  
 Db 1318 GATCGTGTAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377  
 Oy 915 GAGGATCTAGACTTGAATTAAGATGCTACATGACAGCCCTTGAAGAGCTGTAAAG 974  
 Db 1378 GAAGAGATCGTATGAGACTGGAAGAAAGCAACCTGGAAGAGCTGTGAGCTAAAGCT 1437  
 Oy 975 ATTACAGTATTAAGATGACAGATTAATGTTGAAGGTTGAGAAAGTTGAGAGCTATT 1034  
 Db 1438 GTTGATGATCAACAAAGACACACACATCATCATGCTGCTGCTGCTGCTGCTGCTGCT 1497  
 Oy 1035 GCTAACGTAATGCACTGATTAATGCAATTAAGAAACCACTGCTGCTGCTGCTGCTGCT 1094  
 Db 1498 CAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1157  
 Oy 1095 GAAAGACTACAGAAAGCTTGGGCAATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1154  
 Db 1558 GAAAGACTACAGAAAGCTTGGGCAATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617  
 Oy 1155 GCTCAACAGACAGCTTTTAAAGAAATGAAGCTTGCATGAGATGCTTAAAGCT 1214  
 Db 1618 GCTGCTACGAAAGTGAATGAAGAAAGAAAGAGCGCTTGAAGATGCTTCAAGCGG 1677  
 Oy 1215 ACAGTGCACCGCTTGAAGAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1274  
 Db 1678 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1737  
 Oy 1275 ATTGAAGAAAGTACAGCTTGAAGAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1331  
 Db 1738 GCGCTAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1797

Oy 1332 GTGCTTGTGCTCTAGAGAGCCCTGTAGCTCAATTTGCTTAAATGCTGGTACAGGC 1391  
 Db 1798 GCAGTGTGCTGCAATGAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1857  
 Oy 1392 TCCGTAATATGACAGTGTGAAAGAAAGCCCTGAGAGAAAGCTTAAATGCTGACAA 1451  
 Db 1858 TCTGTTGTGCTTAAACCGCTTAAAGCGGCGAGCGCACTAGGTTTCAACGAGCAAC 1917  
 Oy 1452 GGTGAGTGTGATGATGATTAAGACAGAAATCATTTGACCTGCTGCTGCTGCTGCTG 1511  
 Db 1918 GAAGATACGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1977  
 Oy 1512 GCGCTCAAAATGACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1571  
 Db 1978 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2037  
 Oy 1572 AATAAGCTGAACAGCTACGCGAGCGCAAGCAATGCGACAGATGAG 1620  
 Db 2038 GACCTGCGCAAAAGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2086  
 RESULT 5  
 US-09-841-132-380  
 ; Sequence 380, Application US/09841132  
 ; Patent No. US20020061848A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Biactia, Ajay  
 ; APPLICANT: Skelky, Yasir A.W.  
 ; TITLE OF INVENTION: PROST. PETER  
 ; TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION  
 ; FILE REFERENCE: 210121.46968  
 ; CURRENT FILING DATE: US/09/841.132  
 ; NUMBER OF SEQ ID NOS: 399  
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
 ; SEQ ID NO 380  
 ; LENGTH: 1635  
 ; TYPE: DNA  
 ; ORGANISM: Chlamydia pneumoniae  
 US-09-841-132-380  
 Query Match 31.9%; Score 530.4; DB 10; Length 1635;  
 Best Local Similarity 59.5%; Pred. No. 5,2e-120;  
 Matches 957; Conservative 0; Mismatches 636; Indels 15; Gaps 3;  
 Oy 18 GCAAGAAATCAATTTTACAGAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 77  
 Db 7 GCGAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 66  
 Oy 78 TTAGCAGATACCGCAAGTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 137  
 Db 67 CTGCAAGAGCAGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 126  
 Oy 138 GCTTTGCTTCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 197  
 Db 127 AGCTTGTGCTTCCCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 186  
 Oy 198 GAAGATCAATTTTGAAGATGAGCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 257  
 Db 187 GAAGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 246  
 Oy 258 GATATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317  
 Db 247 GACAAAGCAGGCGAGCACTCAACAGCAAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTG 306  
 Oy 318 GCACTAAAAATGAGAGCAGTGTCTTAATGCAATTTGCTGCTGCTGCTGCTGCTGCTG 377  
 Db 307 GCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366  
 Oy 378 GCAACAGCAAGCTGTGAGAGCTTGAAGAGCTTGTCTGCTGCTGCTGCTGCTGCTGCTG 437

Db 367 GCCGTAAAGTTGTTGATGACTCAAAAAATTAGTAACCTGTACACATCAAAA 426  
 Oy 438 GCTATGCTCAGAGTGGCTGAGATATCATCAAGCTCTGA---AAAGTTGAGAGTATATC 494  
 Db 437 GAAATCTCAGAGTACTACTCTACCAAAATAGATATCCGAAATTCGAAATCTTAT 486  
 Oy 495 TCAGAGCTAGAGCGCTGGGCAAGATGTGTATATACATCGCAAGATCTGGAGGT 554  
 Db 487 GCAGAGCTATGAAAAAGTTGGTAAACGATTCATTAAGTGTATGTAACAGCTAAAGGC 546  
 Oy 555 ATGGAACAGCAATGTAAGTGTGTAAGAGCATATTTGACCTGGTATACCTGTCACA 614  
 Db 547 TTGGAACAGCTTTCGACGCTGTAGAGAGATATACATCAACCTGATACCTTCACG 606  
 Oy 615 TACATGTGACAGCAATGAAAAATGGTTGCAGACTTGAATCCCATTTATCTTATC 674  
 Db 607 TACTCTCCCAAAATCCAGAAATCGATGCTTTAGAGACGCTGTGTTCTATC 666  
 Oy 675 ACGATATAAAAGTGTCAAAATCCAGACATTTGGCCACTACTAGTGAAGATCTTTAA 734  
 Db 667 TACGATAAAAAATCTCTGAAATTAAGACTCTTCAGATTTCACACAGTACAGAA 726  
 Oy 735 ACCAACCTCATTAATCTATATTCAGATGATGTGATGTGAGACACTTCAACCTT 794  
 Db 727 TCTGGACGCCCTTTTAATCATTTGCAAGAAATGTAAGAGACCTTTACCACTCTA 786  
 Oy 795 GTCTTGAACAAGATTCTGTGTAATCTTCAATGTGCTGTCACAAAGCGCAGAGATTGT 854  
 Db 787 GTAGTCAATAGACTCGGTGAGAGATTCAGATGTGTGCAAGTGAAGAACTCTGTGTGGT 846  
 Oy 855 GATCGTCGTAAGATGCTTGAAGACATGCTATCTGATGAGAGTGTACAGTATTAACA 914  
 Db 847 GACAGAAAGAAAGCTATGTTAAGACATCGCTATCTTACTGTGGCCAGCATGTTAGC 906  
 Oy 915 GAGGATCTGACATTTAAATTAAGATGCTACAAATGACAGCCCTTGACAGGCTGTAAG 974  
 Db 907 GAAAGAACTGGCATGAACTACAGAAATACACTGCTGATGATTTAGAAAGAACTAGAAA 966  
 Oy 975 ATTACAGTTAAAGTAGCACACTAATTTGTTGAAGTTGAGAGTTACAGAGCTATT 1034  
 Db 967 GTATGCTAGTAAAGAAATATGCAATGCTGTGAAGGCTTAGAAACAACTGATATC 1026  
 Oy 1035 GCTAACCTATTGCACTGATTAATTCGCAATTTGAAACAACTTCTGACTTGAACCT 1094  
 Db 1027 CAAGCTGATCGCAATATTTAAAAACAATGAAAGATACACTTCATGATTAAGCAAA 1086  
 Oy 1095 GAAAACTACAGAGAGTTGGCGAAATTTAGTGTGTGTGAGTGTATTCGTAAGTGA 1154  
 Db 1087 GAAAACTCCAGAGAGGTTTACTTAACCTCCGGGTGTGCGGTATCCGGGTAGGA 1146  
 Oy 1155 GCTCCAGAGAGAGAGCTTTAAAGAAATGAAACTTGCATTTAGAGATGCTTAATGCT 1214  
 Db 1147 GCTGCTACCGAAATAGATGAAAGAAAGAAAGAAAGACAGATGATGACCAACGCA 1206  
 Oy 1215 ACAGCTGACCGCTTGAAGAGATATGCTGTGCTGTGTGAGAAACGACACTTATACGCTT 1274  
 Db 1207 ACCATTGCACTGTGCAAGAGAAATCTCTCCGTGGTGTGAACCTCCCTTGTGCTGT 1266  
 Oy 1275 ATTGAAAAAGTAGAGCTTGTGAGCTTGAG-----GGCAGATGATGCTACTGAGAGCT 1325  
 Db 1267 ATCCCTACACTAGAGCTTTCCTTCATGCTAGAGCAAGCAAGACAGAGCTATGAGTACT 1326  
 Oy 1326 AACATTGCTGCTGCTCTCTAGAGAGCTGTACCTCAAAATCTTTAAATGCTGGGTAC 1385  
 Db 1327 CGATATTATCTTAAAGCATTAACAGCTCCATTAAGCAAAATTCAGTAAGCGAGTAAA 1386  
 Oy 1386 GAAGCTCCGCTAGTATTATGCAAGATGGAAGAACCCCTGAGAGAAAGAGATTAAGCT 1445  
 Db 1387 GAAGGCGCTATCATTTGTACAGAGTTCTAGCAAGATGTCGAAATGAAGAGCTATGATGCT 1446  
 Oy 1446 GCAAGAGGTGAGGTGATGATGATTAAGCAAGATGATGATGATGATGATGATGATGATG 1505  
 Db 1447 TTACGTGACGCTTATACAGATGATGATGATGATGATGATGATGATGATGATGATG 1506

Oy 1506 CGATCAGCGCTTCAAAATGACGCTTCTGACTAGTCTTATTTTACAGAGAGAGT 1565  
 Db 1507 CGCTCAGCTCTGAAAGCGCGCTTCTATCCAGAGATTAATCTCTACAGAGAGAGCTTA 1566  
 Oy 1566 GTGCTAATTAACCTGAA---CCAGCTACGCCAGCGCAGCAATGCCA 1610  
 Db 1567 ATCCGCTATATCCAGAGAGAAATCTTCTACCTCGACGATGCCA 1614  
 RESULT 6  
 US-08-781-986A-266  
 : Sequence 266, Application US/08781986A  
 : Publication No. US2003005436A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Charles Kunsch  
 : TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 : NUMBER OF SEQUENCES: 5255  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Human Genome Sciences, Inc.  
 : STREET: 9410 Key West Avenue  
 : CITY: Rockville  
 : STATE: Maryland  
 : COUNTRY: USA  
 : ZIP: 20850  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
 : COMPUTER: HP Vectra 486/33  
 : OPERATING SYSTEM: MSDOS version 6.2  
 : SOFTWARE: ASCII Text  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/781.986A  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER:  
 : FILING DATE:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Benson, Bob  
 : REGISTRATION NUMBER: 30,446  
 : REFERENCE/DOCKET NUMBER: P8248PP  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (301) 309-8504  
 : TELEFAX: (301) 309-8512  
 : INFORMATION FOR SEQ ID NO: 266:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1017 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : US-08-781-986A-266  
 Query Match 29.18; Score 483.6; DB 7; Length 1017;  
 Best Local Similarity 67.28; Pred. No. 1.2e-108;  
 Matches 681; Conservative 2; Mismatches 331; Indels 0; Gaps 0;  
 Oy 308 TGTTCATGAGAGCTATAAAATGTGACAGAGTGTCTATCCAAATGCTATCGTCGAG 367  
 Db 1 TTTCAGAGAGAGCTTGAATAATGTWCAAGTGTGCGAGGCCAGTGTGTTACGACAGG 60  
 Oy 368 CATGAAACAGCAGACAGACAGCTGTGAAAGCCTTGAAGAGCAATGCTCAACCTGTATC 427  
 Db 61 TATGCAAGAGAGAGTAAAGTGTGTGAAAGGTTACATGAAATTTCTAAAGTTGA 120  
 Oy 428 TGGCAGAGAGAGTATGCTCAGAGTGTGCTGAGATATCATGAGCTCTGAAAGTGGAGA 487  
 Db 121 AATTAATTAATTAATTCGCAAGTGTGCTGATTTAGCAGCAGATATGAAATTTGAGC 180  
 Oy 488 GTATATCTAGAGAGCTATGAGAGCTGTGCGCAACATGCTGTATTCATGCAAGAAATC 547  
 Db 181 TTATATTTGTAGAGCTATGGAAGAGTGTGTAACGATGTGTATTCATTTGAAGAAATC 240  
 Oy 548 TCAGAGTATGAGAAACAGAACTGAAGTGTGAAAGCATGCAATTTGACCTGCTTACT 607

Db 241 AATGAGCTAAACACTGAACTGAAAGGTTGAGATGCAATTTGCAATTTGGTGGTTCG 300  
Oy 608 GTCTCATACATGCTGACAGCAATGAAAAATGGTTGCGACCTTGAAACCATTAT 667  
Db 301 ATCCCGATATATGTTAGTACATGATGATGATGATGATGATGATGATGATGATGAT 360  
Oy 668 CTTAATCAGGATAAAAAGTGCMAATCCAGACATTTTCCACTACTTGTAGAGAGT 727  
Db 361 TTTAGTACAGATGAGAAAAATCTGCTTCCAGATATCTTACCTTATTTAGAACAGT 420  
Oy 728 TCTTAAACCAACCGTCCATTACTATTTATGAGATGATGATGATGATGATGATGATG 787  
Db 421 GGTTCATATCTAATCGCCAACTTAAATGTAGCTGATGATGATGATGATGATGATGAT 480  
Oy 788 AACCTTGTCTTACAGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 847  
Db 481 AATATGCTGCTAAACCGTATGCTGATGATGATGATGATGATGATGATGATGATGAT 540  
Oy 848 ATTTGGTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 907  
Db 541 TTTTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
Oy 908 GATTACAGAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967  
Db 601 GATTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
Oy 968 TGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1027  
Db 661 AAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 720  
Oy 1028 AGCTATTTGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTA 1087  
Db 721 CAGCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Oy 1088 TGACCGTGAAGAACTGACAAAGGTTGGCAAAATTTAGCTGATGATGATGATGAT 1147  
Db 781 TGATCGTGAAGAAATTTACAAAGGCTTACCTAATTTAGCAAGGCTGCTGCTGCTG 840  
Oy 1148 AGTAGAGCTCCAGACAGAGACCTTAAAGAAATTTAGCAAGGCTGCTGCTGCTG 1207  
Db 841 AGTAGAGCTCCAGACAGAGACCTTAAAGAAATTTAGCAAGGCTGCTGCTGCTGCTG 900  
Oy 1208 AATGCTACAGCTGCGACCGTTGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTG 1267  
Db 901 AATGCTACAGCTGCGACCGTTGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCT 960  
Oy 1268 TACGTTATTTGAAAAAGTAGACCTTGTAGCTTGTAGAGGCGATGATGCTACTG 1321  
Db 961 AATGTTTACAAAAAGTAGTAAATTTGAAAGTGAAGCTGAGAGCTGATGAAACAG 1014

## RESULT 7

US-09-738-626-665  
Sequence 665, Application US/09738626  
Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIKOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIRAI, KEIKO  
APPLICANT: TOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAOKO  
APPLICANT: SENOH, AKIHITO  
APPLICANT: IKEDA, MASATO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738, 626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: Patentin ver. 3.0  
SEQ ID NO 665  
LENGTH: 1614  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-665  
Query Match 27.9%; Score 464.2; Db: 9; Length 1614;  
Best Local Similarity 56.4%; Pred. No. 8,4e-104;  
Matches 890; Conservative 0; Mismatches 683; Indels 6; Gaps 1;  
Oy 15 ATGGCAAAAGAAATCAAAATTTTCACAGATGCGCTGCTGCTGCTGCTGCTGCTGCTG 74  
Db 1 ATGGCAAAAGCTAATGCTTTTACCGAGAGCGCCCGAAGGCAATCTCCGGGGGCTGAC 60  
Oy 75 ATGTTAGCAGATACCGCTCAAAAGTAAAGCTTGTGCTTAAAGGGCCCAATGTTGCTTGA 134  
Db 61 GCTCTGGCAAAAGCTGTCAAGGTAAACCTCGGCCACGGCGCGTAACGTGGTCTTGTAT 120  
Oy 135 AAAGCTTTGGTCTCCCTTAATTTACTATGACGGGGTAAACATGCTTAAAGATGCA 194  
Db 121 AAGGCAATCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
Oy 195 TTAGAAAGTCAATTTGAAAGCATGGAGCAAAATTTGCTGCTGCTGCTGCTGCTGCTG 254  
Db 181 CTGAGAGATCTTTTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Oy 255 AATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314  
Db 241 AAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
Oy 315 GAGGACTTAAAAATGTGACAGAGCTGCTAATCCAAATGCTGATCCGTGAGAGCTGAA 374  
Db 301 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Oy 375 ACAGCAAGCAAGCAAGCTGTTGAAGCTTGAAGCAATGCTGCTGCTGCTGCTGCTG 434  
Db 361 GCAGCTGCAAGAAAGCTTGGAGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420  
Oy 435 GAGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494  
Db 421 AAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Oy 495 TCAGAGGCTATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 554  
Db 481 GCTGAGGAGTGAAGAGTTGGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Oy 555 ATGGAAGCAAGCAAGTGAAGTGAAGCAAGTGAAGCAAGTGAAGCAAGTGAAGCAAG 614  
Db 541 ATGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Oy 615 TACATGCTACAGCAATGAAAAATGTTGCAAGCTTGAAGAACCCATTTATCTTAATC 674  
Db 601 TATTTATCTCAACGCAAGCAAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Oy 675 ACGGATAAAAAAGTTCAAAGATCCAGACATTTTGCACACTTACTTGAAGAGCTTAA 734  
Db 661 GTTCCACAAAGATTTCTCCCTCCAGACTTCCCTCATTTGCTGAGAGGTTGGAG 720  
Oy 735 ACCAAGCTCATTTACTATTTATGAGATGATGATGATGATGATGATGATGATGATGATG 794  
Db 721 TCCAGCGTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
Oy 795 GCTTGAAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 854  
Db 781 GTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Oy 855 GATGCTGTAAGCTATGCTTGAAGCAATGCTTATGAGAGCTGCTGCTGCTGCTGCT 914



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Db 841 GACGACGACGACGCTTCATGATGACCTGCTTTCACCAACGCAACGCTGCGAT 900
QY 915 GAGATCTAGACCTGAAATTAAGATGCTACAAATGACAGCCCTTGACAGCTGTAAG 974
Db 901 CCAGATGCGCATCAACCTCAAGAGAGGCTGCGCAAGAGATTTTCGACAGCCGC 960
QY 975 ATTAGCTGATTAAGATAGACAGTAATTTGTAAGGTTGAGAGAGTACAGAGCTAT 1034
Db 961 ATCACTGTTCCAGAGAGAAACCATCATCGTATGATGAGAGGTTCCGAGAAAGCTT 1020
QY 1035 GCTAACGCTTATGACATGATTAATGCAATTAAGAAACAACTGCTGACTTAACCT 1094
Db 1021 GACACAGCTGCGGCGCAATCCCTCCGCAATTCGCAACAGCTGATCCACCTGGTGC 1080
QY 1095 GAAACATACAGAACCTTTGGGGAATTAAGCTGCTGATGCTGATGCTTAAGTGA 1154
Db 1081 GAAAGGCAAGAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1155 GCTCAACAGAGACAGCTTTAAAGAAATGAAACTTCGATTTGAGATGCTTAATGCT 1214
Db 1141 GCACGACGAGAAACGAAAGTCAACGACGCAAGCTGCTGCTGCAAGTCCCAACGCT 1200
QY 1215 ACAGCTGACCCGTTGAGAGATTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1274
Db 1201 GCTGCGCAGCAGCAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1275 ATTA-----AAAGTAGAGCTCTGAGCTTGAAGGCGATGATGCTACTGAGCTAC 1328
Db 1261 GCTGAGACTCTGAGAGCTTACGCGCAAGAGTGAAGGCGCAAGAGGCGCTTGC 1320
QY 1329 ATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1388
Db 1321 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1389 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1448
Db 1381 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1449 ACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1508
Db 1441 ACTTGGAATACGAAACCTGATCAACGAGGTGATGACCCGCAAGTGAACCTAT 1500
QY 1509 TCAGCTTCAAAATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568
Db 1501 TCAGCTTCAAAATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1569 GCTAATTAACCTGAACGAG 1587
Db 1561 GTTGAAGAGCTGCAAGAG 1579

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RESULT 8
US-10-267-311-20
: Sequence 20, Application US/10267311
: Publication No. US2003050469A1
: GENERAL INFORMATION:
: APPLICANT: Sigel, Maryn
: APPLICANT: Chu, R. Randall
: APPLICANT: Mizeen, Lee A.
: TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
: FILE REFERENCE: 12071/002001
: CURRENT APPLICATION NUMBER: US/10/267,311
: PRIOR FILING DATE: 2002-10-09
: PRIOR APPLICATION NUMBER: US/09/613,303
: PRIOR FILING DATE: 2000-07-10
: PRIOR APPLICATION NUMBER: US 60/143,757
: PRIOR FILING DATE: 1999-07-08
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20
: LENGTH: 2847
: TYPE: DNA

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: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: fusion sequence
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(2844)
US-10-267-311-20

Query Match      27.88; Score 461.6; DB 9; Length 2847;
Best Local Similarity 55.98; Prid. No. 4.9e-103;
Matches 878; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

QY 12 CATATGCAAGAAAGAAATCAATTTTCAGCATGCGGCTGCTCCATGCTCGCGAGTT 71
Db 58 CATATGCAAGAAAGAAATGCTAGACAGAAAGAGCGCGCTGCGCTGACGAGGCGCTTG 117
QY 72 GATATGTTACAGATACCGTCAAGATTAAGCTTGGCTCTTAAGGCGCAAGTGTGCTT 131
Db 118 AACGCCCTGCGCGATGCGTAAAGTGATGATGAGGCGCCCAAGGCGCGCAAGTGTGCTG 177
QY 132 GAAAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
Db 178 GAAAGAGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
QY 192 GAATTAAGATATTTTGAAGAAATGGAAGCAAAATTTGCTGCTGAGTGGCTTCAAA 251
Db 238 GAGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
QY 252 ACCATATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
Db 298 ACCGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
QY 312 CATGAGAGCTTAAATATGTAAGAGAGAGGCTGCTAATCAATTTGATTCCTGAGCATT 371
Db 358 GCGAGAGGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
QY 372 GAACAGACAGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
Db 418 GAAAGAGCGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
QY 432 AAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
Db 478 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
QY 492 ATTCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
Db 538 ATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
QY 552 GGTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611
Db 598 ACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 612 CAATACATGCTACAGACATGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
Db 658 GGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
QY 672 ATCAAGGATTAAGAAAGTGTCAAGATCAAGAGCAATTTGCTGCTGCTGCTGCTGCT 731
Db 718 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
QY 732 AAAACCAACCGCTCACTTACTATTAATGAGATGATGATGATGATGATGATGATGATG 791
Db 778 GAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
QY 792 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db 838 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
QY 852 GGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
Db 898 GGGCAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
QY 912 ACAGAGATCTAGACTTGAATTAAGAGATCTAATGATGATGATGATGATGATGATGATG 971

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Wed Apr 16 08:05:36 2003

us-09-001-737-7.rnpb

Page 9

Db	958	AGGGAAGAGCTGGCCCTGACGCGCTGGACACAGCCGACGCTGCGCTGTACGCAAGCCCGC	1017
Oy	972	AAGATTACAGTTGTTAAAGATAGCACAGTATATGTTGAAGGTTACAGAAAGTTCCAGAAAGT	1031
Db	1018	AAAGTCTGTGGTCACACAAGACACAGACCAACCATGTGTGAGGGCCGCGTGTACACGAGCCG	1077
Oy	1032	ATTGCTACCCATATGCACTGATTAAATGCAATTAGAAACACAACTTTCGACTTTGAC	1091
Db	1078	ATCGCGGACAGATGGCCGACGATCGCCAGAGATCTGAGAACAGCACTCCGACTCTACAC	1137
Oy	1092	CGGAAAAACATACAAAGACGTTTGGCAAAATAGTGTTGCTGTACGTATTCAAAAGTA	1151
Db	1138	CGTGAAGAGCTGCAGAGAGGCGCTGGCAAGCTGCGCGTGGTGTGCGGTATCAAGCC	1197
Oy	1152	GSAGCTCCCAACAGACACACTTTAAAGAAATGAACCTTGGCATTAGAGATGCTTAAT	1211
Db	1198	GGTGGCCGACACAGGTGCAGACTCAAGAGGCCAAGCACCGCATGAGAGTGGGTTCG	1257
Oy	1212	GCACACGTGACGCGCTTGAAAGAGTATCGTGTGCTGTGTGGAACAGCACTATTACG	1271
Db	1258	AATGCCAAGGCGCCGCTGAGAGAGGATCTGTCGCGGTGGGGTGTATACCCTGTGGCA	1317
Oy	1272	GTTATTGAAAAGTAGCACACTCTTGAACCTTGAAGGGACATATGCTACGACCTAACCTT	1331
Db	1318	GGGGCCCGACCCCTGCAGCAGACTAAAGCTCGAAGGCCACAGGACACCGGGCCACATC	1377
Oy	1332	GTGCTTCGTGCTAGAGAGACCTGTACGTCAAAATTCCTTTAAATGGGGTTCGAAAGCC	1391
Db	1378	GTGAAGGTGCGCTGTGAGGCCCCGCTGAAGACGATCGCTTCACTCCG98CTGGAACCG	1437
Oy	1392	TCCGAGATTATACAAAGTTAAAAAACCCCTGAGAAAGAAAGATTAATGGTGGACA	1451
Db	1438	GGCGGTGGGCCGAGAAAGTGCCGACACGTGGCCGCTGGCAGCAGACTAACGCTTCAGAC	1487
Oy	1452	GGGAGTGGGTTGATATGATTAATAAGAGAAATCATACCCCTGTCAAGTACAGCATCA	1511
Db	1498	GGTGTCTACAGAGATCTGCTGCTGCCGCGTTGCTGTACCCGGTAAAGGTACCCGGTTCG	1557
Oy	1512	GGCGCTAAAATGACAGCTTCTGTAGCTACTCTATTGTCACAGAGAGAGTGTGCT	1571
Db	1558	GGGCTGCAGAAATCGGCGCTCCATCTGCGGGGCGTTCCTGTACACAGAGGCGCGTGTGCC	1617
Oy	1572	AATTAACCTGA	1583
Db	1618	GACACGCCGGA	1629

RESULT 9  
 US-10-267-311-28  
 Sequence 28, Application no US10267311  
 Publication No. US20030050469A1  
 GENERAL INFORMATION:  
 APPLICANT: Siegel, Marvin  
 APPLICANT: Chiu, N. Randall  
 APPLICANT: Mizzen, Lee A.  
 TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO  
 FILE REFERENCE: 12071/002001  
 CURRENT APPLICATION NUMBER: US/10/267,311  
 CURRENT FILING DATE: 2002-10-09  
 PRIOR APPLICATION NUMBER: US/09/613,303  
 PRIOR FILING DATE: 2000-07-10  
 PRIOR APPLICATION NUMBER: US 60/143,757  
 PRIOR FILING DATE: 1999-07-08  
 NUMBER OF SEQ ID NOS: 55  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 28  
 LENGTH: 1947  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: fusion sequence  
 FEATURE:  
 FEATURE:

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? NAME/KEY: CDS
? LOCATION: (1)... (1944)
US-10-267-311.28

Query Match      27.7%   Score 460: DB 9: Length 1947:
Best Local Similarity 55.8%   Pedit No. 9 9e-10:
Matches 877: Conservative 0: Mismatches 695: Indels 0: Gaps 0

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QY	12	CATATGCAAAAGAAATCAAAATTTTCACCAATACCGCGCTGCCATGCTGCGCGAGATT	71
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Db	322	CACATGCGCCAAACAAATATGGCTACGACGMAAGGCCCGCTGCGGCTCGAGGGGGCTTG	381
QY	72	GATATGTTGACGATACCTCCGCAACATGAACTGGTCTCTAAAGGGCGCAATGTGTTCT	121
QY	132	GAAGAAAGCTTTTGGTCTCCCTTAATTCTAATACGGGGTAACCATTTGCTAAAGATC	191
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Db	442	GAAGAAAGCTGGGGGCGCCCAACGATATCCAAAGATGGTGTGTCTATCGCCCAAGAGATC	501
QY	192	GAATTAGAAGATCATTTTGAACAAATGGGAGCAAAATTTGGTGTCTGAAGTGGCTTCTAA	251
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Db	502	GACCTGGAGATCCGTACGAGAAAGATTCGGGCCCGACCTGGTCTCAAGAGGTAGCCAAAG	561
QY	252	ACCAATGATATTGCTGGTGTATGGGAGCACTACTGCACAGTTTGGAGACAAAGCATTTGT	311
		111111 111111 111111 111111 111111 111111 111111 111111 111111 111111	
Db	562	ACCGATGAGCTGCGCGGTACGGCACACAGCAGCGCCACCGGTGTGCGCCAGGGCGTTGGT	621
QY	312	CATGAAGAGCAATAAAATGTGACACAGTGTCTAATCCAAATTTGGTATTCGTGAGAGCAT	371
		111111 111111 111111 111111 111111 111111 111111 111111 111111 111111	
Db	622	CCGAGAGCGCTGCGCCCAACGTCCGCGCGCGGCCAACCGCGCTGGTCTCAAGACGGCGATC	681
QY	372	GAACACGCAACAGCAACGCTGTGAAGCCGTGAAGAGCATTTGGTGTCAACCTGTATCTGGC	431
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Db	682	GAAGAGCGCGTGTGAGAAAGGTATCAACCGAACCTCTCTCAAGGGCGCCAAAGAGTGTCAAGC	741
QY	432	AAGCAAGCATTTGGTGTGCGTGGCTGCGTCAAGTATCATCAAGCTGTGAAGAAAGTTGGAGATAT	491
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Db	742	AAGAGACAAATTTGGGCGCACCCACACATTTTCGGGGGAGCACAGTCCATCTGGTGTACCTG	801
QY	492	ATCTCAGAACTATGAGACGCTGTGGGCACAGATGTGTGTAATTCATCGAAGAAATCTCGA	551
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Db	802	ATGCGGAGGGGATGAGCAAGGTGGCAACGAGGGCGTCAACCTGTCAAGAGAGTCCAAC	861
QY	552	GGTATGGAACAGAACTTGAAGTGTGAAGGACATCAAAATTTGACAGCTGTACTCTCT	611
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Db	862	ACCTTTGGGCTGCAAGCTGTCAAGTCAACGAGAGGTATGCGGTTCCGCAAGGGCTACATCTCC	921
QY	612	CAATACATGTGTACACAGACATGAAGAAATGGTTGCGAGACCTTGAAAGAACCATTAATCTTA	671
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Db	922	GAGTACTTCTGTGACCAACCCGGAGAGCTCAAGAGGGCGTCTCGAGAGAACCCCTACATCTCG	981
QY	672	ATCAGCGATTAAGAAATGTGCAAAATCCAGAGACATTTTGGCCACACTTGTAGAGAAAGTCTT	731
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Db	982	CTGTGTCACTCAAGAGTGTCCACTGTCAAGATCTGTGCGCGCTGTGAGAAAGTCAATC	1041
QY	732	AAAGCAACAGCTGCATTATCTTAATTGACAGATATGTGAGATGTGTATGTATGACACTTCACAC	791
		111111 111111 111111 111111 111111 111111 111111 111111 111111 111111	
Db	1042	GAGAGCGGTAAAGCCGCTGCTGATCATGGCGAGAGACGTCAAGGGCGAGGGCTCTCCAC	1101
QY	792	CTTGTCTTGAACAAGATTGTGTGATCTTCAATGTGTGTGTCTCAAGGCCCGAGATT	851
		111111 111111 111111 111111 111111 111111 111111 111111 111111 111111	
Db	1102	CTGTGCTGCAACAAGATCCGGGCACTTCAATGGTGTGGCGGTCAAGGGCTCCGGGCTTC	1161
		111111 111111 111111 111111 111111 111111 111111 111111 111111 111111	
QY	852	GGTATGCTGTAAACATCTATCTTGAAGACATTTGCTATCTTCAAGGTGTGTGACAGTGTAT	911
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Db	1162	GCGGACCGCGCCGAAGCGCATGTCTGACAGATATGTGTGCAATCTTCCACGGGTGTCAAGTATTC	1221
QY	912	ACAGAGCATCTAGGACTTGAATTTAAAGATGCTACATATGACAGCCCTTGGAGAGGCTGCT	971
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Db	1222	ACCGAAGAGGTCTGCGCTGACCTGTGAAACGCCGACCTGTCTGTGTAGGCAAGTTCAGAGCT	1281
QY	972	AAGATTACAGTTGATTAAGATAGCACATTAATTTGTTAAAGTTTCAGAGAAATTTCAGAGCT	1031

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Db 1282 AAGCTGCTGTCACACAGAGAGACACCATCTGTCAGAGGCGCCGAGACCGAGCC 1341
Oy 1032 ATTGCTAACGCTATTGCACTGATTAATGCAATTAGAAACAACACTTGTGACTTGCAC 1091
Db 1342 ATGCGGAGAGAGTGGCCGAGATCCGCGAGATCCGAGAACAGAGACTCCGACTACGAC 1401
Oy 1092 CGTGAAGAACTACAGAAAGCTTTGGCGAAATTAAGTGGTGTGAGTGTATCAAGTA 1151
Db 1402 CTGTGAAGAGCTGAGAGAGGCGGCGCAAGCTGGCGGCTGTGTGCGGCTATCAAGGCG 1461
Oy 1152 GAGAGCTCAACAGAGACAGCTTTAAAGAAATGAAAGTGGCAATGAGATGCTTAAT 1211
Db 1462 GGTGCGGCGACAGAGTGAAGTCAAGAGAGCGCAACCGCATGAGAGATGGGCTTGC 1521
Oy 1212 GGTACAGGTGACCGGTGAGAGATGCTGTGCTGTGTGTGCAACAGCACTTATTAG 1271
Db 1522 AATGCAAGGCGCCCTCGAGAGGAGCATGCTGCGCGGTGGGTGTGAGCTGTGCA 1581
Oy 1272 GTTATGAAAGATGACAGCTCTTGAAGCTTGAAGGCGCATGATGCTACTGAGCTAAC 1331
Db 1582 GCGGCGCGGACCGCTGAGAGCTGAAGCTGAAGGCGAGAGGCGACCGCGGAGATC 1641
Oy 1332 GTGCTGCTCTCTGTAAGAGAGCTGTAAGCTTAATGCTGTGAGAGAGC 1391
Db 1642 GTGAAGGTGCGCTGAGAGGCGCCGCTGAAGAGATCCCTTCACTCCGCGGTGAGCG 1701
Oy 1392 TCCGTAATTTGACAAAGTTGAAAGACCCCTGACAGAAAGATTTAATGCTGACAA 1451
Db 1702 GCGGCTGTGCGCGAGAGAGTGCACAACTGCGCGCTGCGACGAGAGTGAAGCTGAG 1761
Oy 1452 GGTGAGTGGTGTATGATTAATTAAGAGATCAATGACCTGTCAAGATTAAGAGATCA 1511
Db 1762 GGTGCTACAGAGATCTGCTGCGCGGCTGTCTACCGCGGTGAAGGTGAGCGGTTG 1821
Oy 1512 GCGCTTAAGAAATGCAAGCTTCTGTAAGTATTTTGAAGAGAGAGTGTGCT 1571
Db 1822 GCGCTGAGAAATGCGCGCTCATGCGGCGGTGTCTGACACAGAGGCGCTGTGCTGC 1881
Oy 1572 AATAAACCCTGAA 1583
Db 1882 GACAAGCGGAA 1893

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RESULT 10
US-09-712-363-23
Sequence 23 Application US/09712363
Patent No. US20020164388A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rolstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12

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; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

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Query Match 27.6%, Score 458.6, DB 9, Length 1623:
Best Local Similarly 55.8%, Pred. No. 2e-102:
Matches 875: Conservative 0; Mismatches 694; Indels 0; Gaps 0;

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Db 1 ATGGCCAAAGAAATTCGCTACGACAGAGAGCCCGCTCCGCGCTGAGAGGCGGCTTGAAC 60
Oy 75 ATGTAGACAGATACCGCTCAAGATTAAGCTTGGTCTTAAGAGGCGCAATGGTCTTGA 134
Db 61 GCCCTGCGCGATCGGTAAAGTGAATGAGTGGCCCAAGAGGCGCGCAAGCTGCTTGGA 120
Oy 135 AAGGCTTTGGTCTCCCTTAATTAATGACGGGGTACACATGCTTAAGAGATTTGAA 194
Db 121 AAGAAAGTGGGTGCGCCCGACGATCACCACGATGATGTGTCTCATCCCAAGAGATGAG 180
Oy 195 TAGAAGATGATTTGAAACATGAGCAAAATTTGTCTGAAGTGGCTTTGAAGC 254
Db 181 CTGAGAGATTCCTGACGAGAAATGCGCGAGCTGTCAAAAGAGTGAAGCAAGAGACC 240
Oy 255 AATGATATGCTGTGATGAGAGACATCTGCAACAGTTTGAACAGAGCCATTGTCAT 314
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Oy 315 GAAGACTTAAAGATGTGACAGAGGTGCTAATCCAAATGATATCCGTGAGAGATTGAA 374
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Oy 375 ACAGCAAGCAAGCAAGCTGTGAAGGCTTGAAGGCAATGCTCAACATGATCTGCAAG 434
Db 361 AAGGCGCTGAGAGAGTGCACCGAGACCTGCTCAAGGCGCGCAAGAGTGAAGAGCAAG 420
Oy 435 GAAGCTATTGCTAGGTCGCTGACAGTATCATGAGCTGTGAAGATTTGAGAGTATATC 494
Db 421 GAGCGATTTGCGGCGCACCGGAGATTTGCGGCGGTGACCAAGTCCATGAGTACATGAC 480
Oy 495 TCAGAGCTTGAAGCGGTGGGCAAGGATGATGATTAACATGAGAGATTCAGAGT 554
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Db 601 TACTTGTGACCGACCGGAGCGCTCAGAGCGGTCTGAGAGACCCCTCATATCTGTG 660
Oy 675 ACGGATAAAGAAAGTCAACATCAAGCATTTTGGCACTACTGAGAGATTTTAA 734
Db 661 GTCACTCCCAAGGTCTCCACTGTCAAGGATCTGCTGCGCTGTGAAAGGATTCGGA 720
Oy 735 ACAAACCGCTCATTAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGAT 794
Db 721 GCCGCTAGCGCTCTGATCATCGCGCGAGAGCTGAGAGGCGGCTGTGCAACCTG 780
Oy 795 GCTCTGAACAATTCGTGATTTCAATTAATGATGATGATGATGATGATGATGATGATGAT 854
Db 781 GTCTTCAACAATTCGCGGACCTTCAAGTGGGTGATGATGATGATGATGATGATGATGATGAT 840
Oy 855 GATGCTGTGAAGCTATGCTTGAAGCATTTCTTGAAGGTGTGATGATGATGATGATGAT 914
Db 841 GACCGCGGAGAGCGATGCTGAGATATGACATTCATCCGCTGTGATGATGATGATGATGAT 900

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QY 975 ATACAGTGAATTAAGTACAGAGTAAATTTGTAAGCTTCAAGAGTTCAGAGCTATT 1034
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Db 961 GTCTGTGTACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1035 GCTAACGCTATTGCTGATTAATGCAATTTAGAAACAACTGCTTGTGACTTACCTG 1094
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Db 1021 GCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1095 GAAACCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1154
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Db 1081 GAGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1155 GCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1214
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Db 1201 GCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
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QY 1395 GTAGTATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1454
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Db 1381 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1445 GAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1514
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Db 1441 GTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1515 CTCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1574
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Db 1501 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1575 AAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
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Db 1561 AAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1569

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US-10-267-311-16
Query Match 27.6% Score 458.6; DB 9; Length 1920;
Best Local Similarity 55.8%; Pred No. 2; 2e-102;
Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

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Db 1 ATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 75 ATGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 134
  || || || || || || || || || || || || || || || || || || || || ||
Db 61 GCCCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 135 AAGGCTTGTCTCTCCCTTAATTACTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
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Db 121 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 195 TTGAGAGAGATGTTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
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Db 181 CTGAGAGAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 255 AATGATATTGCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
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Db 241 GATGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 315 GAGGAGCTAATAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
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Db 301 GAGGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 375 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434
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Db 361 AAGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 435 GAGAGCTTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494
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Db 421 GAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 495 TCAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554
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QY 555 ATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 614
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QY 675 ACGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 734
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QY 735 ACAGAGAGCTGATCTATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794
  || || || || || || || || || || || || || || || || || || || || ||
Db 721 GCCGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 795 GTCGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
  || || || || || || || || || || || || || || || || || || || || ||
Db 781 GTCGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 855 GATGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
  || || || || || || || || || || || || || || || || || || || || ||
Db 841 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 915 GAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 974
  || || || || || || || || || || || || || || || || || || || || ||
Db 901 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 975 ATTAAGTGAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1034
  || || || || || || || || || || || || || || || || || || || || ||
Db 961 GTCTGTGTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020

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0y	1035	GCACACCCATTATGACATGGATTAAATCCCAATTAGAAACAAACACTTCBACCTTACCTGGACCG	1094
0y	1021	GCCGACACAGAGGCCACAGATCCGCCACGAAATCGAAGAACAGCCAGCTCCGACATACGACCG	1080
0y	1095	GAAGAAATCACAAAGACGTTTGGCGAAATTAGCGGTGTGTAGCTTATTCAAGTAGGA	1154
0y	1081	GAAAGCTCGCAGAGCGGTGCGCAACCTGCGCGGTGTGTCCGGTATCAAGCCCGT	1140
0y	1155	GCTCCACAGAGACACCTTTAAAGAAATGAACCTCGCATTAGATAGCTCTAAATGCT	1214
0y	1141	GCGCGCACCGAGGTGCAACTCAAGAGCCGAAACACCCATCGAGATTCGGTCCAT	1200
0y	1215	ACACGTGAGCGCTTAAAGAAAGTATCGTTGCTGGTGTGGAACAGCACTTATTACGTT	1274
0y	1201	GCCAAAGCGCGCTCGCAGSAGGCAATGTGCCGTGGGGGTGTACAGCTGTTCAGAACG	1260
0y	1275	ATTGAAATAGACACACTCTTACCTTAGAGGCGATATGCTACTGACGTACATCTTG	1334
0y	1261	GCCCCAGCCCTGGACAGCTGAACCTGAAAGCGACAGGCGACCGGGCCACCAATCTGTG	1320
0y	1335	CTTCTGCTCTAAGAACAGCTGTACGTCAATTGCTTTAAATCTGTGGTACGAAGGCTCC	1394
0y	1321	AAGCTGCGCTGAGAGGCCCTCCGTCAAGCAAGATGCTCTCAACTCGCGGCTGTGAACCGGCG	1380
0y	1395	GTAAGTATTAGCAACTTTGAAGAAACAGCCCTCGCAGAACAGGATTTATGTCTGCACAGCT	1454
0y	1381	GTGTGTGCGCGAAGATGTGGCAACACTTCGCGGTGCGCACGGAATGAACGCTCAACACCGGT	1440
0y	1455	GAGTGGGTATATATGATTTAAACAGGAAATCATTTGACCCGTCTCAAAATACAGCATAGCG	1514
0y	1441	GTCTACAGGAGATGTGTCTGCTGCGCGGGGTGTCTGACCCCGTTCAAAAGGTATACCCGTTGGCG	1500
0y	1515	CTTCAAAATCAGCTTCTGTAGTACTCTTAATTTTGGACAACAGAGCAGTGTGTGTAAAT	1574
0y	1501	CTGCAAGAAATCGGCGTTCATCGCGGGGTGTTCCCTGACACCGCAGGCGCGTGTGGCGAC	1560
0y	1575	AAACCTGAA	1583
0y	1561	AAGCCGAA	1569

RESULT 13  
US-09-738

US-09-738-626-1/c  
; Sequence 1, Application US/09738626  
; Publication No. US20020197605A1  
; Journal Information

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
ADDRESSEE: MRD STUSS

APPLICANT: ANDO, SEIRO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: ONUMA, TOSIO

APPLICANT: UCHIAL, KEIKO  
; YOKOI, HARUHIKO  
APPLICANT: MATSUOKA, MIYUKI

APPLICANT: IREDA, MASATO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IRIEISHI, NAOKU

APPLICANT: OZAKI, AKIO

FILE OF INVESTIGATION: NOVELL FOLIOCCOLOIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: NS/09/739 636

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988

; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059

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; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1

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; LENGTH: 3309400
; TYPE: DNA

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ORGANISM: *Corynebacterium glutamicum*

US-09-738-626-1

Query Match	27.68;	Score 458.4;	DB 9;	Length 3509400;
Best Local Similarity	56.48;	Pred. No. 1.2e-100;		
Matches 905; Conservative	0;	Mismatches 681;	Indels 18;	Gaps 2

QY 12 CATATGGCAAAAGAAATCTCAAAATTTTTCACAGATATCCGGTGTGCATATGTCGGCCAGAGTT 71  
 Db 289043 CACATGGCAAAAGATCATGCGCTTATGAGAAAGACACTGTGTGCTAGAAAGAGGACTG 289048  
 QY 72 GATATGTTAGCAGATACCTCCAAAGTACGCGTGTCTTAAAGGGCCGACATGTTGTTCT 131  
 Db 2890483 AACACCTGGCTACGCTGTTAAAGGTTACTTTGGACCAAAAGGGCCGTAAACGCTGTTTG 2890424  
 QY 132 GAAAAGCGTTTGGTTCCTCCCTTAATTAATATACGGGGTAAACATTTCTTAAAGATC 191  
 Db 2890423 GAAAAGCGTTGGGGTGCCCAACACATTTACAAAGATGTTGTACACATGCAACGCTAGATC 2890364  
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 Db 2890363 GACCTTGGAGATCTCTTACGAAAGATGCGGACAGGCTGTGTACAAAGAAAGTGTCTTAAAG 2890304  
 QY 252 AACCATGATATTTGCTGTGATGGAGACACTGTGCAACAGTTTGTACACAGCCATTGTT 311  
 Db 2890303 AACTGTGAGCTGCGGGCGATATGGACACACACGCGTACCCTATTTGGCACAGCGCTGTGTT 2890244  
 QY 312 CATGAAGACATAAAAAATGTAGACAGCAGGCTCTATATCATTTGGTATCTCGTGCAGCATT 371  
 Db 2890243 CCGGAAGAGCCCTGCGGCACAGCTTGTCTGCTCTTAACCCAAATGGCGCATAGCCTGGCATC 2890184  
 QY 372 GAACACGACACAGCAACAGCTGTTTGAAGCTTTGAAAGCCATTGCTCAACCTGATGTGAC 431  
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 QY 432 AAGAAAGCTATTTCTCAGTGGCGGAGATCATACGCTGTGAAAAGTTGGAGAGAT 491  
 Db 2890123 GAGAGAGCATGTGCTGTACCCGTGTGATCTCCGAGCTATGCCACAGCTATCCGCGCCACAG 2890064  
 QY 492 ATCTCAGAGCTATGAGAGCGTGGGG - - - - - CAGCATGGTGTGATTTAC 536  
 Db 2890063 ATTCTAGAGCAATTTACGATGTGCGGCTGGGCAAGCTGAACAGATTTCCGTCATCT 2890004  
 QY 537 ATCGAAGATCTCGAAGTATGGAACAGACTGGAAGTGTGAGAGCCTAATTTAC 596  
 Db 2890003 GTTGAAGAGTCACACACTTTCGAGTTGAGCTGAGGTTCTGAGAGGATATGCGCTTTGAT 2889944  
 QY 597 CGTGGTACCTGTCTCAATACATGATGTCACAGACAAATGAATAAAATGTTGCAGACTTGA 656  
 Db 2889943 AAGGGCTACACTTCGGGTTCTCTCCAAACGACATGAGAGCGGCTGAGGCTGTCTGGAA 2889884  
 QY 657 AACCAATTATCTTAATACAGCATATAAAAGTGTCAAACTGTCAACAAATATTTGGCCACTA 716  
 Db 2889883 GATCTTACATCTCTGCTGTGTTTCCGGCAAAATCACTCAACATCAAGACCTGCTCCACTG 2889824  
 QY 717 CTGAGAGAGTCTTAAACCAACGCTCATTTACTCATTTATGCAAGATGTGAGATGTT 776  
 Db 2889823 CTGAGAGAGGTATGACAGTCCGGCAACCTTTGTGATCTGTCGAGAGACGCGAGGG 2889764  
 QY 777 GAAGCACTTCCACCTCTTGTGGAACAAGTTCGAGTACTTTTCAATGGTGGTGGTGC 836  
 Db 2889763 GAGGCTGTCTCCACCGCTGGTGTCAACAAAGATCGTGGACCTTGAAGTCTGTGCTGTT 2889704  
 QY 837 AAAGGCGCAGATTTGGTGTATGCTGTAAAGCTATGCTGTAAAGATTTGCTATCTGACA 896  
 Db 2889703 AAGGCTCCGGGCTTGGCAGCCGCTGTAAAGCTCAGCTGAGAGCATTTGTTGTAC 2889644  
 QY 897 GGTGTACATGATTTACAGAGATCTAGACCTTGAATTTAAAGATCTTCAATGACAGCC 956  
 Db 2889643 GGTGTACATGATTTCTGAAAGATTTGGGCTCTCTCTTGAACCGGTGATCTGACACTT 2889584  
 QY 957 CTGGAACAGGCTCTTAAATTTACAGTTGATTAAGATACCAAGTAATTTGTTGAAGTTCA 1016  
 Db 2889583 CTAGGCGACGACGCAAGGCTTTGTGTACCAAGATATACACCACTGCTGTATGCGGGCA 2889524

D	503	TTGTTAACGCCAAGACAAATTGGCGTACACCAAGAGAGCCCGTCGCGGCGCTCGAGCGGGGCT	562
Q	70	TTGATATTTAGCAGATTAACCGTCAAAATACAGCTTGGTCTTAAAGGGCCCAATGTTGTC	129
D	563	TGAAAGCCCTCGCGGATGGCGTAAAGGTACATTTGGGCCCCAAGAGGCCCAAGTGTCC	622
Q	130	TTGAAAAAGCTTTGGATTCTCCCTTAATTTCTAATGACGGGGTAAACCATTTGTTAAAGTA	189
D	623	TGAAAAAAGATGGGGTGGCCCCACGATCAACCAAGATGTGTGTCTCATTCGCMAAGAGA	662
Q	190	TGCAATTTGAAGATCACTTTTGAAACATGGGAGCAAAATTTGGTGTCTGAAGGGCTCTA	249
D	683	TGAGCTGTGAGATCCGTACAGAAAGATCGGGCCGACCTGTCTAAAGGTAGCAGA	742
Q	250	AAGCAATGATTTGGTGTATGTGGACCACTTACTGCAACGTTTGGACACAGCATTTG	309
D	743	AACCGGATGACGTCCCGGTGACGGACACACAGCCGCAACCGCTGTGCGCCAGGGGTTGG	802
Q	310	TTTCATGAGACTAAAAAATGTGACACGAGGTGCTAATCCAAATTTGATTCGCTGAGGA	369
D	803	TTGCGAGAGCGCTGCGCAACCTCGCGCGGGGCCAACCCGCTGGTCTCAAAAGCGGCA	862
Q	370	TTGAAACGCAACGCAACAGCACTGTGTAAGCCCTTGAAGCCATTTGTCMAACCTGATCTG	429
D	863	TGAAAAAGGCGGTGGAGAAGGTACCGAGACCTCTCTAAGGGCGCCAAAGAGGTGAGA	922
Q	430	GCAAGGAGCTATTGGCTAGGTCGCTGCTGCACTATCATACGCTGTGAAAAAGTGGAGAT	489
D	923	CCAAAGGACGATTTGGCGCCACCCGACACCAATTTGCGGGGTGACACGTCATCGGTACC	982
Q	490	ATATCTAGAGAGTATGAGAGGTGTGGGCAAGAGTGTGTGATTAATCAATGAAATCTC	549
D	983	TGATGCGCGAGGAGATGAGCAAGGTGGGCAAGAGGGGTATCACCGTCGAGAGTCCA	1042
Q	550	GAGGATGAGAAACAGACCTTAAGTGGTTTGAAGGATATGCAATTTGACGTTGACTACTGT	609
D	1043	ACACCTTGGGCTGCGAGCTGCAGCTCACGAGAGATATGGCGTTGCAAGAGGCTACATCT	1102
Q	610	CTCAATCATGATGTCACACACAAATGAAAAATGGTTGCGACCTTGAAAAACCATTTACT	669
D	1103	CGGGGTACTTCGTGAGCCACCCGAGACCGTCAGAGGGGTCTCTGAGAGACCTTCAATCTC	1162
Q	670	TAAACACGGATTAATAAATGTCAACATCCAAAGACATTTTGCCTACTTGAAGAACTTC	729
D	1165	TGCTGTGACTCTCAAGGTGTCTCAGTGAAGATCTGTGCGCTGTCTGAAAGGTCA	1222
Q	730	TTAAACACACCGCTCCATTACTCATTTATTCAGATGATGTGATGGTGAAGCACTTCCA	789
D	1223	TGGAGCGGGTAAAGCGCTGTATATGCGCGAGGACGTGAGGGCCAGGCGCTGTCCA	1282
Q	790	CCCTTGTCTTGAACAAGATTCTGTGTACTTTCATATGTGTGTCTGCAAGCGCCAGGAT	849
D	1283	CCCTGTGCTCAACAAGATCCGGGGACCTTCATAGTGGTGGGGTCAAGAGCTCCGGCT	1342
Q	850	TTGGTGTGCTGTAAACCTATGCTTGAAGACATTTGTAATCTTGAACAGTGTACAGTGA	909
D	1343	TGGCGAGCGCCGCAAGGCAATCTCAGAGATATGGCCATTCTCAACCGGTGTAGGTGA	1402
Q	910	TTACAGAGATCTAGACATTTGAATTTAAAGATGTCAATAGACAGCCCTTGGAAGAGTG	969
D	1403	TCACCGAAGAGTCCGCTCGACCTGGAAGAACCGGCACTGTGCGGTAGCAAGGCC	1466
Q	970	CTAGATTTACGTTGATTAAGATGAGCAAGTAATTTGTTGAAGTTCCAGAAAGTTCCAG	1022
D	1463	GCAAGGTGTGTGCCAAGAGCAAGAACACACATCTGTCAAGGGCCCGGTGACCCAGC	1522
Q	1030	CTATGTGTAAACGTTATGCACTGATTAATGTGGCAATTAGAAACAACATCTTGACTTTG	1088
D	1523	CCATCCGCGGAGATGAGTGGCCCAATCCGCAAGAGATCTGAAACAGCACTCCGACTTACG	1582
Q	1090	ACCGTGAATACTACAGAAAGTTTGGCGAAATTAAGTGTGGTGTAGCTGTATTAAAG	1149





